## **RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:

Source:

Date Processed by STIC:

ENTERED



PCT

RAW SEQUENCE LISTING DATE: 01/25/2005
PATENT APPLICATION: US/10/521,053 TIME: 09:21:38

Input Set : A:\P1943R1 PCT Sequence Listing.txt

Output Set: N:\CRF4\01252005\J521053.raw

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3 <110> APPLICANT: PHILLIPS, HEIDI S.
      5 <120> TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
             Treatment of Tumor
      8 <130> FILE REFERENCE: P1943R1-PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/521,053
C--> 11 <141> CURRENT FILING DATE: 2004-12-20
     13 <150> PRIOR APPLICATION NUMBER: US 60/394,998
     14 <151> PRIOR FILING DATE: 2002-07-09
     16 <160> NUMBER OF SEQ ID NOS: 4
     18 <210> SEQ ID NO: 1
     19 <211> LENGTH: 939
     20 <212> TYPE: DNA
     21 <213> ORGANISM: Homo sapiens
     23 <400> SEQUENCE: 1
     24 teggeegaga tgtetegete egtggeetta getgtgeteg egetaetete 50
     26 tetttetgge etggaggeta tecagegtae tecaaagatt caggtttaet 100
     28 cacqtcatcc agcagagaat ggaaagtcaa atttcctgaa ttgctatgtg 150
     30 tctqqqtttc atccatccga cattgaagtt gacttactga agaatggaga 200
     32 gagaattgaa aaagtggagc attcagactt gtctttcagc aaggactggt 250
        ctttctatct cttgtactac actgaattca ccccactga aaaagatgag 300
     36 tatgcctgcc gtgtgaacca tgtgactttg tcacagccca agatagttaa 350
     38 gtgggatcga gacatgtaag cagcatcatg gaggtttgaa gatgccgcat 400
     40 ttggattgga tgaattccaa attctgcttg cttgcttttt aatattgata 450
     42 tgcttataca cttacacttt atgcacaaaa tgtagggtta taataatgtt 500
     44 aacatggaca tgatcttctt tataattcta ctttgagtgc tgtctccatg 550
       tttgatgtat ctgagcaggt tgctccacag gtagctctag gagggctggc 600
     48 aacttagagg tggggagcag agaattetet tatecaacat caacatettg 650
     50 gtcagatttg aactcttcaa tctcttgcac tcaaagcttg ttaagatagt 700
     52 taagcgtgca taagttaact tccaatttac atactctgct tagaatttgg 750
     54 gggaaaattt agaaatataa ttgacaggat tattggaaat ttgttataat 800
     56 gaatgaaaca ttttgtcata taagattcat atttacttct tatacatttg 850
     58 ataaaqtaaq qcatqqttgt ggttaatctg gtttattttt gttccacaag 900
     60 ttaaataaat cataaaactt gaaaaaaaaa aaaaaaaaa 939
     62 <210> SEO ID NO: 2
     63 <211> LENGTH: 119
     64 <212> TYPE: PRT
     65 <213> ORGANISM: Homo sapiens
     67 <400> SEQUENCE: 2
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     68
     69
     71
        Ser Gly Leu Glu Ala Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr
     72
                                              25
                          20
       Ser Arg His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys
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45
75
77
   Tyr Val Ser Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu
78
   Lys Asn Gly Glu Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser
80
                                                             75
81
                     65
                                         70
83
   Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe
84
                     80
                                         85
   Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn His Val
86
                                        100
                                                            105
87
                     95
89
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90
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93 <211> LENGTH: 1440
94 <212> TYPE: DNA
95 <213> ORGANISM: Homo sapiens
97 <400> SEQUENCE: 3
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102 tecegeecea ggtegteete teageatggg ggteeegegg ceteageeet 150
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     agccacctct ccctcctgta ccaccttacc gcggtgtcct cgcctgcccc 250
106
108
    ggggactect geettetggg tgteeggetg getgggeeeg cageagtace 300
110
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112 tgggaaaacc aggtgtcctg gtattgggag aaagagacca cagatctgag 400
114 gatcaaggag aagctctttc tggaagcttt caaagctttg gggggaaaag 450
116 gtccctacac tctgcagggc ctgctgggct gtgaactggg ccctgacaac 500
118 accteqqtqc ccaccqccaa gttcqccctg aacggcgagg agttcatgaa 550
    tttcgacctc aagcagggca cctggggtgg ggactggccc gaggccctgg 600
120
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122
124
     accttectge tattetectg eecgeacege etgegggage acctggagag 700
126
     gggccgcgga aacctggagt ggaaggagcc cccctccatg cgcctgaagg 750
     cccgacccag cagccctggc ttttccgtgc ttacctgcag cgccttctcc 800
128
    ttetaceete eggagetgea aetteggtte etgeggaatg ggetggeege 850
130
    tggcaccggc cagggtgact tcggccccaa cagtgacgga tccttccacg 900
132
134
    cctcgtcgtc actaacagtc aaaagtggcg atgagcacca ctactgctgc 950
136 attgtgcagc acgcggggct ggcgcagccc ctcagggtgg agctggaatc 1000
138
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140
    tactcacggc agcggctgta ggaggagctc tgttgtggag aaggatgagg 1100
142
    agtgggctgc cagccccttg gatctccctt cgtggagacg acaccggggt 1150
144
     cctcctgccc accccagggg aggcccagga tgctgatttg aaggatgtaa 1200
    atgtgattcc agccaccgcc tgaccatccg ccattccgac tgctaaaagc 1250
    gaatgtagtc aggccccttt catgctgtga gacctcctgg aacactggca 1300
148
     tctctgagcc tccagaaggg gttctgggcc tagttgtcct ccctctggag 1350
150
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156 <210> SEQ ID NO: 4
157 <211> LENGTH: 365
158 <212> TYPE: PRT
159 <213> ORGANISM: Homo sapiens
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161	<400> SEQUENCE: 4														
162	Met	Gly	Val	Pro	Arg	Pro	Gln	Pro	Trp	Ala	Leu	Gly	Leu	Leu	Leu
163	1				5					10					15
165	Phe	Leu	Leu	Pro	Gly	Ser	Leu	Gly	Ala	Glu	Ser	His	Leu	Ser	Leu
166					20					25					30
168	Leu	Tyr	His	Leu	Thr	Ala	Val	Ser	Ser	Pro	Ala	Pro	Gly	Thr	Pro
169					35					40					45
171	Ala	Phe	$\mathtt{Trp}$	Val	Ser	Gly	Trp	Leu	Gly	Pro	Gln	Gln	Tyr	Leu	
172					50		_	_		55					60
174	$\mathtt{Tyr}$	Asn	Ser	Leu	. –	Gly	Glu	Ala	Glu		Cys	Gly	Ala	Trp	
175	_		_		65	_		_	_	70	_	~-		_,	75
177	Trp	Glu	Asn	GIn		Ser	Trp	Tyr	Trp		Lys	Glu	Thr	Thr	
178	_	_		_	80	_	_	-1	-	85		-1	_		90
180	ьeu	Arg	Ile	гла		гуѕ	ьeu	Pne	ьeu		Ата	Pne	гÀг	Ата	
181	<b>a</b> 1	<b>a</b> 1	T	<b>~1</b>	95	TT	mla sa	T	~1 <del>-</del> -	100	T	T	<b>~1</b>	C	105
183	GIĀ	GIĀ	Lys	GIY	110	TAL	THE	ьeu	GIII	115	ьeu	ьeu	GIA	cys	120
184 186	T 011	C1	Pro	7 cm		The	C0~	17-1	Dro		ת דת	Tira	Dho	- ר ת	
187	пеп	GIY	PIO	лэр	125	1111	261	vai	PIU	130	AIA	шуъ	FIIC	ліа	135
189	Δen	Glv	Glu	Glu		Met	Δsn	Phe	Asn		Lvc	Gln	Glv	Thr	
190	71011	O <sub>T</sub>	OLU	O L u	140	1100	11011	1110	1101	145	<b>1</b> 175	0111	O <sub>1</sub>		150
192	Glv	Glv	Asp	Trp		Glu	Ala	Leu	Ala		Ser	Gln	Ara	Trp	
193	0_1	0-1	р		155					160		0	3		165
195	Gln	Gln	Asp	Lys	Ala	Ala	Asn	Lys	Glu		Thr	Phe	Leu	Leu	
196			-	•	170			•		175					180
198	Ser	Cys	Pro	His	Arg	Leu	Arg	Glu	His	Leu	Glu	Arg	Gly	Arg	Gly
199		_			185		_			190		_			195
201	Asn	Leu	Glu	Trp	Lys	Glu	Pro	Pro	Ser	Met	Arg	Leu	Lys	Ala	Arg
202					200					205					210
204	Pro	Ser	Ser	Pro	Gly	Phe	Ser	Val	Leu	Thr	Cys	Ser	Ala	Phe	Ser
205					215					220					225
207	Phe	Tyr	Pro	Pro		Leu	Gln	Leu	Arg		Leu	Arg	Asn	Gly	
208	_	_	_	_	230	_			_	235					240
210	Ala	Ala	Gly	Thr		Gln	Gly	Asp	Phe	_	Pro	Asn	Ser	Asp	_
211	_	_,			245	_	_	_		250	_	_		_	255
213	Ser	Pne	His	Ala		Ser	ser	Leu	Thr		гàг	Ser	GIY	Asp	
214	774 -	***		<b>0</b>	260	<b>T</b> 1.	77-7	<b>~1</b>	772	265	<b>01.</b> -	Ŧ	27-	<b>~</b> 1	270
216	HIS	HIS	Tyr	Cys	_	тте	vai	GIII	HIS		GIY	Leu	Ala	GIN	
217 219	Lou	7~~	Val	C1.,	275	C1.,	Sor	Dro	ת דת	280	C0~	Cox	17-1	T 011	285
220	пец	Arg	vai	GIU	290	GIU	Ser	PIO		295	ser	Set	vai	neu	300
222	Val	Glv	Ile	Val		Glv	Val	T.011			ሞh r	Δla	Δla	בומ	
223	VAI	GIY	11C	val	305	GIY	val	Leu	Leu	310	T 11T	лта	Ата	AIG	315
225	Glv	Glv	Ala	Len		Trn	Ara	Ara	Met		Ser	Glv	Leu	Pro	
226	1	1			320	~~₽	3	3		325		- I			330
228	Pro	Trp	Ile	Ser		Ara	Glv	Asp	asp		Glv	Val	Leu	Leu	
229		- <b>- P</b>			335	5	1			340	1				345
231	Thr	Pro	Gly	Glu		Gln	asp	Ala	Asp		Lys	Asp	Val	Asn	
232			•		350		•		-	355	-	•			360

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234 Ile Pro Ala Thr Ala 235 365 VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date